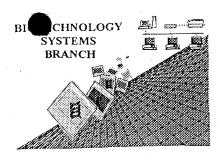# RAW SEQUENCE LISTING
# ERROR REPORT

*O4C0*
*03/07/01*

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/780,113*

Source: *OIPE*

Date Processed by STIC: *3-8-01*

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**
**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**
**PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)**
**PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)**

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
**http://www.uspto.gov/web/offices/pac/checker**

OIPE

RAW SEQUENCE LISTING           DATE: 03/08/2001
PATENT APPLICATION: US/09/780,113    TIME: 11:49:51

Input Set : A:\#1041801 v1 - 50681-20001.txt
Output Set: N:\CRF3\03082001\I780113.raw

*Does Not Comply
Corrected Diskette Needed*

```
   3 <110> APPLICANT: TYRRELL, JOHN V.
   4         BERGQUIST, PATRICIA R.
   5         BERGQUIST, PETER L.
   6         SCHOLIN, CHRISTOPHER A.
   8 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING RAPHIDOPHYTES
  10 <130> FILE REFERENCE: 50681200121
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/780,113
C--> 13 <141> CURRENT FILING DATE: 2001-02-09
  15 <150> PRIOR APPLICATION NUMBER: 09/596,136
  17 <151> PRIOR FILING DATE: 2000-06-16
  20 <160> NUMBER OF SEQ ID NOS: 30
  22 <170> SOFTWARE: PatentIn Ver. 2.1


ERRORED SEQUENCES

  90 <210> SEQ ID NO: 5
  91 <211> LENGTH: 18
  92 <212> TYPE: DNA
  93 <213> ORGANISM: Artificial Sequence
  95 <220> FEATURE:
  96 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificial
  98 <220> FEATURE:
  99 <223> OTHER INFORMATION: olignucleotide probe
 101 <400> SEQUENCE: 5
E--> 102 gcatgttgaa acgctccag
 315 <210> SEQ ID NO: 20
 316 <211> LENGTH: 21
 317 <212> TYPE: DNA
 318 <213> ORGANISM: Artificial Sequence
 320 <220> FEATURE:
 321 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificial
 323 <220> FEATURE:
 324 <223> OTHER INFORMATION: olignucleotide probe
E--> 326 <400> SEQUENCE: 25
E--> 327 tcatctttcc ctcacggtac ttgtt              25
 486 <210> SEQ ID NO: 30
 487 <211> LENGTH: 20
 488 <212> TYPE: DNA
 489 <213> ORGANISM: Artificial Sequence
 491 <220> FEATURE:
 492 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificial
 494         PCR Primer
 496 <400> SEQUENCE: 30
C--> 497 ccttggtccg tgtttcaaga              20
E--> 507 1
```

*Handwritten annotations:*

*Number of bases differ:*
*- 18 listed*
*- 19 shown*
*move to here*
*19*

*- 21 listed*
*- 25 shown*
*21?*
*move to here.*

*Delete extraneous numeral from the end of the file. It is causing an invalid base count for sequence #30.*

VERIFICATION SUMMARY
PATENT APPLICATION:   US/09/780,113

DATE:  03/08/2001
TIME:  11:49:53

Input Set : A:\#1041801 v1 - 50681-20001.txt
Output Set: N:\CRF3\03082001\I780113.raw

```
L:12  M:270 C: Current Application Number differs, Replaced Current Application Number
L:13  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:39  M:112 C: (48) String data converted to lower case,
L:57  M:112 C: (48) String data converted to lower case,
L:72  M:112 C: (48) String data converted to lower case,
L:87  M:112 C: (48) String data converted to lower case,
L:102 M:112 C: (48) String data converted to lower case,
L:102 M:252 E: No. of Seq. differs, <211>LENGTH:Input:18 Found:19 SEQ:5
L:117 M:112 C: (48) String data converted to lower case,
L:132 M:112 C: (48) String data converted to lower case,
L:147 M:112 C: (48) String data converted to lower case,
L:162 M:112 C: (48) String data converted to lower case,
L:177 M:112 C: (48) String data converted to lower case,
L:192 M:112 C: (48) String data converted to lower case,
L:207 M:112 C: (48) String data converted to lower case,
L:222 M:112 C: (48) String data converted to lower case,
L:237 M:112 C: (48) String data converted to lower case,
L:252 M:112 C: (48) String data converted to lower case,
L:267 M:112 C: (48) String data converted to lower case,
L:282 M:112 C: (48) String data converted to lower case,
L:297 M:112 C: (48) String data converted to lower case,
L:312 M:112 C: (48) String data converted to lower case,
L:326 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:25
L:327 M:112 C: (48) String data converted to lower case,
L:327 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:25 SEQ:20
L:342 M:112 C: (48) String data converted to lower case,
L:357 M:112 C: (48) String data converted to lower case,
L:369 M:112 C: (48) String data converted to lower case,
L:378 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=24
L:398 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=25
L:418 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=26
L:438 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=27
L:458 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=28
L:483 M:112 C: (48) String data converted to lower case,
L:497 M:112 C: (48) String data converted to lower case,
L:507 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:20 SEQ:30
```